



STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/813,156A
Source: J. F. W. P.
Date Processed by STIC: 11/6/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER** **VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary



ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/813,156A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
(OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
(NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWO

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/813,156A

DATE: 11/06/2006
TIME: 10:52:22

Input Set : A:\Q80880.ST25.txt
Output Set : N:\CRF4\11062006\J813156A.raw

3 <110> APPLICANT: Council Of Scientific & Industrial Research
4 Singh, Jagmohan
5 Kumar, Raj
7 <120> TITLE OF INVENTION: Novel Temperature Regulated Promoters and Expression Vectors

For

8 Proteins From Schizosaccharomyces Pombe
10 <130> FILE REFERENCE: Q80880
12 <140> CURRENT APPLICATION NUMBER: US 10/813,156A
13 <141> CURRENT FILING DATE: 2004-03-31
15 <160> NUMBER OF SEQ ID NOS: 3
17 <170> SOFTWARE: PatentIn version 3.3
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 185
21 <212> TYPE: DNA
22 <213> ORGANISM: nmt-185 promoter
24 <400> SEQUENCE: 1

Does Not Comply
Corrected Diskette Needed
(pg.1)

25 aaaggaatcc gattgtcatt cggcaatgtg cagcgaaact aaaaaccgga taatggacct
27 gttaatcgaa acattgaaga tatataaagg aagaggaatc ctggcatatc atcaattgaa
29 taagtgtaat taattatttc aatctcattc tcactttctg acttatagtc gctttgttaa
31 atcat

60
120
180
185

See
item #

34 <210> SEQ ID NO: 2
35 <211> LENGTH: 146
36 <212> TYPE: DNA
37 <213> ORGANISM: nmt-146 promoter
39 <400> SEQUENCE: 2

40 taaaaaccgg ataattggacc tggttaatcga aacattgaag atatataaag gaagaggaat
42 cctggcatat catcaattga ataagttgaa ttaattattt caatctcatt ctcactttct
44 gacttatagt cgctttgtta aatcat
47 <210> SEQ ID NO: 3
48 <211> LENGTH: 1199
49 <212> TYPE: DNA
50 <213> ORGANISM: nmt1 promoter
52 <400> SEQUENCE: 3

60
120
146

10 on
error
Summary
Sheet.

53 tgatcagaaa attatcgcca taaaagacag aataagtcac cagcggttgt ttcatttcct
55 atattttttt tttatttttt ttttttttaa taagggaataa tttacgtct aaggatacag
57 aagattgtta gcacattaaa gtaataaagg ctttaagtagt aagtgctta gcatgttatt
59 gtatttcaaa ggacataatc taaaataata acaatatcat ttctcacaag ttattcaatt
61 ttcttttttt ttcttaataa tatcaagaat gtattatttg ttgacataa gtcaactaat
63 ttatttaata tgctggatta atcttgacga catgtaaatt aacaagtttt agtcaaataa
65 cggtgaagtt tcaatgaact caaataattt ctcttttttt ttaataaacc atatgtctaa
67 tctgatttat attttccgca ggatcaactg aagttatgac atttgattg gatcacttat
69 aaccttggtc gccaaataat acaaaaatca gcgttataaa acaagaagg tttttgttaa
71 gaaattaate ctctttcttg ataagaaagt tgaaccgaaa ttgcagatac tgatatatga
73 aaataatacc cacaattttg ggaatagcgc aagcctcaat ttaacaataa ggtgaggaca

60
120
180
240
300
360
420
480
540
600
660

YI
213 responses CAN only be either Artificial/Unknown
OR Genus/Species.

file:///C:/CRF4/Outhold/VsrJ813156A.htm

11/6/2006

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75	catgataatg	acctcaatga	ttgttagaag	aaaagagcct	cattacaaaa	tcgaaaaatg	720
77	aatgggtggg	tacaagtttc	caaaacatgg	taaagtggac	tttgcgatg	agacgtaaat	780
79	agaaaaaaac	acttggtata	tgttttctag	aattattgtt	gtctctttat	ggttggatga	840
81	tgcaaaatag	taatttcggt	tagttgctgt	aaaacaccac	gagacaaata	gatatggata	900
83	tttattaaat	caggaaaaac	gtaactctcg	gctactggat	ggttcagtca	cccaacgatt	960
85	actggggaga	gaaaacaggg	caaaagcaaa	gcttaaagga	atccgattgt	cattcggcaa	1020
87	tgtgcagcga	aactaaaaac	cggataatgg	acctgttaat	cgaaacattg	aagatatata	1080
89	aaggaagagg	aatcctggca	tatcatcaat	tgaataagtt	gaattaatta	tttcaatctc	1140
91	attctcactt	tctgacttat	agtcgctttg	ttaaatacatg	tctactaaca	agatcactt	1199

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